

I. AMENDMENTS

Please cancel claims 29 to 32 and 39 to 100 without prejudice. Upon entry of the present amendment, the status of the claims will be as follows:

1. (Original) A method for inferring a trait of a bovine subject from a nucleic acid sample of the bovine subject, comprising identifying in the nucleic acid sample, at least one nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait, thereby inferring the trait.
2. (Original) The method of claim 1, wherein the nucleotide occurrence of at least 2 of the SNPs is determined to infer the trait.
3. (Original) The method of claim 2, wherein the nucleotide occurrences of the at least 2 SNPs comprise a haplotype allele, and wherein the method infers the trait using the identified haplotype allele.
4. (Original) The method of claim 2, wherein the at least 2 SNPs are related by dominance and/or epistasis.
5. (Original) The method of claim 4, further comprising identifying a diploid pair of haplotype alleles and inferring the trait using the diploid pair of haplotype alleles.

6. (Original) The method of claim 1, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, a milk quality susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, or susceptibility to infection with and shedding of pathogens.

7. (Original) The method of claim 6, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

8. (Original) The method of claim 7, wherein the trait is fat thickness.

9. (Original) The method of claim 8, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high fat thickness.

10. (Original) The method of claim 8, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low fat thickness.

11. (Original) The method of claim 7, wherein the trait is retail yield.

12. (Original) The method of claim 11, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high retail yield.

13. (Original) The method of claim 11, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low retail yield.

14. (Original) The method of claim 7, wherein the trait is tenderness.

15. (Original) The method of claim 14, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high tenderness.

16. (Original) The method of claim 14, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low tenderness.

17. (Original) The method of claim 7, wherein the trait is marbling.

18. (Original) The method of claim 17, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with more abundant marbling.

19. (Original) The method of claim 17, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with less abundant marbling.

20. (Original) The method of claim 7, wherein the trait is average daily gain.

21. (Original) The method of claim 20, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with a high daily gain.

22. (Original) The method of claim 20, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low daily gain.

23. (Original) A method for determining a nucleotide occurrence of a polymorphism in a bovine sample, comprising:

a) contacting a bovine polynucleotide in the sample with an oligonucleotide that binds to a target region of any one of SEQ ID NOS:24493 to 64886, wherein the target region comprises a position corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982 or wherein the target region is within 3000 nucleotides of a nucleotide corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, and

b) determining the nucleotide occurrence of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, wherein the determination comprises analyzing binding of the oligonucleotide or detecting an amplification product generated using the oligonucleotide, thereby determining the nucleotide occurrence of the polymorphism.

24. (Original) The method of claim 23, wherein the oligonucleotide binds to a target sequence that comprises one of the SNPs and the nucleotide occurrence is determined based on the binding of the oligonucleotide to the target sequence.

25. (Original) The method of claim 23, wherein the bovine polynucleotide is contacted with a pair of oligonucleotides that comprise a primer pair, and the nucleotide occurrence is determined using an amplification product generated using the primer pair.

26. (Original) The method of claim 23, wherein the terminal nucleotide of the oligonucleotide binds to the SNP.

27. (Original) The method of claim 25, wherein the polynucleotide is contacted with a pair of oligonucleotides each comprising a different detectable label.

28. (Original) The method of claim 27, wherein the terminal nucleotide of each oligonucleotide pair is complementary to a different nucleotide at position 300 of any one of SEQ ID NOS:19473 to 21982, or a complement thereof.

29 to 32. (Cancelled).

33. (Original) A method for identifying a bovine single nucleotide polymorphism (SNP) associated with a trait, comprising identifying a test SNP that is in disequilibrium with a SNP position corresponding to position 300 of one of SEQ ID NOS:19473 to 21982.

34. (Original) The method of claim 33, wherein the test SNP is in a target region of a bovine genome, wherein the target region is within about 500,000 nucleotides from a SNP position corresponding to position 300 of one of SEQ ID NOS:19473 to 21982.

35. (Original) The method of claim 34, wherein the target region consists of at least 20 contiguous nucleotides of SEQ ID NOS:24493 to 64886.

36. (Original) The method of claim 34, wherein the target region consists of at least 20 contiguous nucleotides of SEQ ID NOS:19473 to 21982.

37. (Original) The method of claim 33, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, susceptibility to infection with or shedding of pathogens.

38. (Original) The method of claim 37, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

39 to 100 (Cancelled).